

SEQUENCE LISTING

<110> McCallum, Claire  
Slade, Ann J.  
Colbert, Trent  
Knauf, Vic  
Anawah Inc.

<120> Tomatoes Having Reduced Polygalacturonase Activity Caused by Non-  
Transgenic Mutations in the Polygalacturonase Gene

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accgttagat aaatggtcaa ttttgaaccc aaaagtggat gagaaggta ttttagagcc	900		
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caaactaata taatacccat tacaattaac catattgacc aactcaaacc ccttaaaatc	1380		
tataaataga caaacccttc ccatacctct tatcataaaa aaaataataa tctttttcaa	1440		
tagacaagtt taaaaccat accatataac aatatac atg gtt atc caa agg aat	1496		
Met Val Ile Gln Arg Asn			
1	5		
agt att ctc ctt ctc att att att ttt gct tca tca att tca act tgt	1544		
Ser Ile Leu Leu Ile Ile Ile Phe Ala Ser Ser Ile Ser Thr Cys			
10	15	20	
aga agc aat gtt att gat gac aat tta ttc aaa caa gtt tat gat aat	1592		
Arg Ser Asn Val Ile Asp Asp Asn Leu Phe Lys Gln Val Tyr Asp Asn			
25	30	35	
att ctt gaa caa gaa ttt gct cat gat ttt caa gct tat ctt tct tat	1640		
Ile Leu Glu Gln Glu Phe Ala His Asp Phe Gln Ala Tyr Leu Ser Tyr			
40	45	50	
ttg agc aaa aat att gaa agc aac aat aat att gac aag gtt gat aaa	1688		
Leu Ser Lys Asn Ile Glu Ser Asn Asn Ile Asp Lys Val Asp Lys			
55	60	65	70
aat ggg att aaa gtg att aat gta ctt agc ttt gga gct aag ggt gat	1736		
Asn Gly Ile Lys Val Ile Asn Val Leu Ser Phe Gly Ala Lys Gly Asp			
75	80	85	
gga aaa aca tat gat aat att gtaagtattt aaatattgga atatatttgt	1787		
Gly Lys Thr Tyr Asp Asn Ile			
90			
ggggatgaaa atgatagaga atataagaat tatttggaaag gatgaaaagt tatattttat	1847		
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Ser Asp Tyr Lys Asp Arg Arg Leu Trp Ile Ala Phe Asp Ser Val Gln			
150	155	160	
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Asn Leu Val Val Gly Gly Gly Thr Ile Asn Gly Asn Gly Gln Val			
165	170	175	180
tgg tgg cca agt tct tgc aaa ata aat aaa tca ctg gtaattttat		3501	
Trp Trp Pro Ser Ser Cys Lys Ile Asn Lys Ser Leu			
185	190		
aaccttgctt ataagttta cgctatgtg ctgcattct ttaaacttgt tctaaagata		3561	
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Pro Cys Arg Asp Ala Pro Thr			
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actttgtatt taaatattaa aactaatatt gtttaatttt cag gcc tta acc ttc		4271	
Ala Leu Thr Phe			
200			
tgg aat tgc aaa aat ttg aaa gtg aat aat cta aag agt aaa aat gca		4319	
Trp Asn Cys Lys Asn Leu Lys Val Asn Asn Leu Lys Ser Lys Asn Ala			
205	210	215	
caa caa att cat atc aaa ttt gag tca tgc act aat gtt gta gct tca		4367	
Gln Gln Ile His Ile Lys Phe Glu Ser Cys Thr Asn Val Val Ala Ser			
220	225	230	235
aat ttg atg atc aat gct tca gca aag agc cca aat act gat gga gtc		4415	
Asn Leu Met Ile Asn Ala Ser Ala Lys Ser Pro Asn Thr Asp Gly Val			
240	245	250	
caa gta tca aat act caa tat att caa ata tct gat act att att gga		4463	
Gln Val Ser Asn Thr Gln Tyr Ile Gln Ile Ser Asp Thr Ile Ile Gly			
255	260	265	

aca g gtttatttat ttaattttta ttatccaat ttaatttagaa aaaaaaagga	4517	
Thr		
gtatTTTtat ttgataacta aattattaat tttaatttt ttttatagt gt gat gat	4574	
	Gly Asp Asp	
	270	
tgt att tca att gtt tct gga tct caa aat gtg cag gcc aca aat att	4622	
Cys Ile Ser Ile Val Ser Gly Ser Gln Asn Val Gln Ala Thr Asn Ile		
275	280	285
act tgt ggt cca ggt cat ggt ata ag gtactctatt ttacaaat	4668	
Thr Cys Gly Pro Gly His Gly Ile Ser		
290	295	
acttggcc atttctcta ttccataaaa ggtatgtatgataataatt actttaatc	4728	
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tatTTTct ctTTTtatTT ttccatggat tac t att gga agc tta gga tct	5620	
	Ile Gly Ser Leu Gly Ser	
	300	
gga aat tca gaa gct tat gtg tct aat gtt act gta aat gaa gcc aaa	5668	
Gly Asn Ser Glu Ala Tyr Val Ser Asn Val Thr Val Asn Glu Ala Lys		
305	310	315
att atc ggt gcc gaa aat gga gtt agg atc aag act tgg cag	5710	
Ile Ile Gly Ala Glu Asn Gly Val Arg Ile Lys Thr Trp Gln		
320	325	330



415	420	425	
tgc aaa aat gtc cat ttt aac aat gct gaa cat gtt aca cca cac tgc Cys Lys Asn Val His Phe Asn Asn Ala Glu His Val Thr Pro His Cys 430	435	440	7000
act tca cta gaa att tca gag gat gaa gct ctt ttg tat aat tat Thr Ser Leu Glu Ile Ser Glu Asp Glu Ala Leu Leu Tyr Asn Tyr 445	450	455	7045
taatttatac tatagatctt caatatatac cagatatgtat atatcacaat aaacaaatct atatctatgt attgaataat tattattaat atgtacggat tgaagttta ataaagactac tatgtatttc tattttctag tcaaaagttt gacgattgtat cttttatg tacaaaaata ataaaatggt tatttatatg atgtatataat cccttggta tttcttggta aactataatg tcattattta ataaactatta tctgtgcaat gattgtat tttatgata cataatataat ctttcatcat tgataataag aataaaatat tttacgtcta ttactttgtg aatttatatgt agattttagt ttttggta tttttaatata accgagtga aatataaaga g			7105 7165 7225 7285 7345 7405 7456

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Ser Ser Ile Ser Thr Cys Arg Ser Asn Val Ile Asp Asp Asn Leu Phe  
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Lys Gln Val Tyr Asp Asn Ile Leu Glu Gln Glu Phe Ala His Asp Phe  
 35 40 45

Gln Ala Tyr Leu Ser Tyr Leu Ser Lys Asn Ile Glu Ser Asn Asn Asn  
 50 55 60

Ile Asp Lys Val Asp Lys Asn Gly Ile Lys Val Ile Asn Val Leu Ser  
 65 70 75 80

Phe Gly Ala Lys Gly Asp Gly Lys Thr Tyr Asp Asn Ile Ala Phe Glu  
 85 90 95

Gln Ala Trp Asn Glu Ala Cys Ser Ser Arg Thr Pro Val Gln Phe Val

100 105 110

Val Pro Lys Asn Lys Asn Tyr Leu Leu Lys Gln Ile Thr Phe Ser Gly  
115 120 125

Pro Cys Arg Ser Ser Ile Ser Val Lys Ile Phe Gly Ser Leu Glu Ala  
130 135 140

Ser Ser Lys Ile Ser Asp Tyr Lys Asp Arg Arg Leu Trp Ile Ala Phe  
145 150 155 160

Asp Ser Val Gln Asn Leu Val Val Gly Gly Gly Thr Ile Asn Gly  
165 170 175

Asn Gly Gln Val Trp Trp Pro Ser Ser Cys Lys Ile Asn Lys Ser Leu  
180 185 190

Pro Cys Arg Asp Ala Pro Thr Ala Leu Thr Phe Trp Asn Cys Lys Asn  
195 200 205

Leu Lys Val Asn Asn Leu Lys Ser Lys Asn Ala Gln Gln Ile His Ile  
210 215 220

Lys Phe Glu Ser Cys Thr Asn Val Val Ala Ser Asn Leu Met Ile Asn  
225 230 235 240

Ala Ser Ala Lys Ser Pro Asn Thr Asp Gly Val Gln Val Ser Asn Thr  
245 250 255

Gln Tyr Ile Gln Ile Ser Asp Thr Ile Ile Gly Thr Gly Asp Asp Cys  
260 265 270

Ile Ser Ile Val Ser Gly Ser Gln Asn Val Gln Ala Thr Asn Ile Thr  
275 280 285

Cys Gly Pro Gly His Gly Ile Ser Ile Gly Ser Leu Gly Ser Gly Asn  
290 295 300

Ser Glu Ala Tyr Val Ser Asn Val Thr Val Asn Glu Ala Lys Ile Ile  
305 310 315 320

Gly Ala Glu Asn Gly Val Arg Ile Lys Thr Trp Gln Gly Gly Ser Gly  
325 330 335

Gln Ala Ser Asn Ile Lys Phe Leu Asn Val Glu Met Gln Asp Val Lys  
340 345 350

Tyr Pro Ile Ile Ile Asp Gln Asn Tyr Cys Asp Arg Val Glu Pro Cys  
355 360 365

Ile Gln Gln Phe Ser Ala Val Gln Val Lys Asn Val Val Tyr Glu Asn  
370 375 380

Ile Lys Gly Thr Ser Ala Thr Lys Val Ala Ile Lys Phe Asp Cys Ser  
385 390 395 400

Thr Asn Phe Pro Cys Glu Gly Ile Ile Met Glu Asn Ile Asn Leu Val  
405 410 415

Gly Glu Ser Gly Lys Pro Ser Glu Ala Thr Cys Lys Asn Val His Phe  
420 425 430

Asn Asn Ala Glu His Val Thr Pro His Cys Thr Ser Leu Glu Ile Ser  
435 440 445

Glu Asp Glu Ala Leu Leu Tyr Asn Tyr  
450 455